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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT	1
LOCUS	AF140273
DEFINITION	Ichthyophthirius multifiliis immobilization antigen precursor (TAG48) gene, complete cds.
ACCESSION	AF140273
VERSION	AF140273.1 GI:4888370
KEYWORDS	Ichthyophthirius multifiliis
SOURCE	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Ophryoglenina; Ichthyophthiriliidae.
ORGANISM	
REFERENCE	1 (bases 1 to 2446)
AUTHORS	Clark,T.G., Lin,T.L., Jackwood,D.A., Sherrill,J., Lin,Y. and Dickerson,H.W.

RESULT 2
 ICYIMANT
 LOCUS ICHTHYOPHTHIRIUS MULTIFILIIS mRNA linear INV 18-SEP-1998
 DEFINITION mRNA, partial cds.
 ACCESSION M92907
 VERSION M92907.1 GI:3628568
 KEYWORDS Ichthyophthirius multifiliis.
 ORGANISM Ichthyophthirius multifiliis.
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Ophryoglenina; Ichthyophthirius.
 REFERENCE 1 (bases 1 to 1249)
 AUTHORS Lin,T.L. and Dickerson,H.W.
 TITLE Purification and partial characterization of immobilization
 antigens from Ichthyophthirius multifiliis
 JOURNAL J. Protozool. 39 (4), 457-463 (1992)
 PMID 1383510
 PUBLMED 2 (bases 1 to 1249)
 AUTHORS Clark,T.G., McGraw,R.A. and Dickerson H.W.
 TITLE Developmental expression of surface antigen genes in the parasitic
 ciliate Ichthyophthirius multifiliis
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (14), 6363-6367 (1992)
 MEDLINE 1631132
 PUBLMED 3 (bases 1 to 1249)
 AUTHORS Clark,T.
 TITLE Direct Submission
 JOURNAL Submitted (18-SEP-1998) Microbiology and Immunology, Cornell
 University, Ithaca, NY 14853, USA
 REMARK Sequence update by submitter
 On Sep 18, 1998 this sequence version replaced gi:159289.
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 Db 1 GAGCGTTCCATGCTGTGATTGACTTAAGCTGGATTGACTGATGTTGCTT 60
 Qy 116 CTGATCTTGACTTGTGTTAATTCGACCTTAATTTACTATAATGGTGTGCTT 175
 Db 61 CTGATCTTGACTTGTGTTAATTCGACCTTAATTTACTATAATGGTGTGCTT 120
 Qy 176 AAGGAGAAAGCTAANGTAATTAACCTTTCGACCAAAATATGCTGTAAGCTATATGTG 235
 Db 121 AAGGAGAAAGCTAATGTTAATTAACCTTTCGACCAAAATATGCTGTAAGCTATATGTG 180
 Qy 236 TACCATGCCAAATAAACAGTAGGCTGTGTTACCATGCAAGTGTACTTTAG 295
 Db 181 TACCATGCCAAATAAACAGTAGGCTGTGTTACCATGCAAGTGTACTTTAG 240
 Qy 296 CCACATTAATGCGACTTAACTGGCCTACTGGCACCTGACTTGTGACTTGTGACAGATG 355
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 .. Qy 356 TTTCATGATGATCAGCCGATAAATGCTTTAACCTTACTATAATGGTGTG 415
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 Qy 416 GTTCCTCCCTTAAGGTGAACCTCTGGCTTTAAGTTTGTGCTGTCGTCGCCTGCAG 475
 Db 361 GTTCCTCCCTTAAGGTGAACCTCTGGCTTTAAGTTTGTGCTGTCGTCGCCTGCAG 420
 Qy 476 GTGTTGCGTGCCTGACTAGTAAATGCTTACCTGTTACCTGTTACCTGCTCTCTCTG 535
 Db 421 GTGTTGCGTGCCTGACTAGTAAATGCTTACCTGTTACCTGCTCTCTCTG 480
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 Qy 776 GCCAAATAAACAAAAGGATTCCTGCCACTGCAAGTGCTTAAGCTAAATTTGCCACAT 835
 Db 721 GCCAAATAAACAAAAGGATTCCTGCCACTGCAAGTGCTTAAGCTAAATTTGCCACAT 780
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 Db 781 AATGCACTAACCTTAATGCTTCACTGCGACTGACTGACTGTTTTAATGGTAAATCG 901
 Qy 896 GAAATGCTCACATATGTTCTTAATGCAATTGTTAATGGTAAATCG 955
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 Qy 956 AAGCAGGTTAAAGTTATGTTAAAGTGTCAAGTAAGTAAACTACTCCAGCACATGCCTC 1015
 Db 901 AAGCAGGTTAAAGTTATGTTAAAGTGTCAAGTCAGGGAGTGAACCTGTTTTA 960
 Qy 1016 CAGGTAAATACTGCTACTTAAGCCACATAATGTTGACCCATGTCCTGTTGCAAGTAC 1075
 Db 961 CAGGTAAATACTGCTACTTAAGCCACATAATGTTGACCCATGTCCTGTTGCAAGTAC 1020

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Qy	1195	TGTACTAAAAATTAACTCTGGGCCAGCTAAAGTATGCTGAAGCTACTCAAAA	1254	Mismatches 394; Indels 111;	
Db	1289	TGTTCTAAAAATTAACTCTGGCTTACAGCTAAAGTATGCTGAAGCTACTCAAAA	1348	Qy 167 GTGCTGCTTAAGGAGAAGCTAATGGTAATTAACCTTTCGCAGCAAATAATGGCTAGAG 226	
Qy	1255	GTATAATGCCCTTCACTACTTGCTAAATTATGATTGCTGAGCTACTTAAAA	1314	Db 1673 GTGCTAATGTTAGAAATTATTATGAAATGTCACATTGCTGCTA 1732	
Db	1349	GCATATGCCCAAGTTCACATTGGCAAAATTATGCTAAATGCTTCT 1408		Qy 227 GATAATGTTACCATGCCAAATAACAGAGTAGGCTCTGTTACCAATGCGTAGTTAG 286	
Qy	1315	TTCTATTATTG 1326		Db 1733 GTCATGACAGCTGTCGGTAAACAGAGTGGTGTGCAATTGCTGTAATGCCG 1792	
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RESULT 4				Db 1793 CTACCATAGTCGATTAATGTCGCTTACTGACTGAGCTGATGATGGAG 1852	
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DEFINITION	Ichthyophthirius multifiliis	immobilization antigen isoform		Db 1853 TAATCTACTGTTAGATCATTCACAGAAATGTTAAATGACACTAACTTTTACT 1912	
ACCESSION	AF324424	complete cds.		Qy 407 ATATGGTGGTTCTCTTAAGGTGAACCTCCCTGGCTTAAGTTTGCTGCTGCTG 466	
VERSION	AF324424.1	GI:12698726		Db 1913 ATAATGTTAAATGGTAAATCTCCCTCAATCCAGTAAAGTAAATGCAACCTGTC 1972	
KEYWORDS				Qy 467 CGGTGCGAGGTGGTGCCTCCGGTTACTAGTTAATGTTAACTGGTACCTGGCTACCTGGAC 526	
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ORGANISM	Ichthyophthirius multifiliis			Qy 527 ATTCTCTGGCCATGCAAGGTGCCTAAGCTAATTGCCCATAATGTTAATGGTC 586	
		Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;		Db 1994 TTGTTAAGCTACTTGTGTAATGATGCTCAATAACGGCATATAATGTAACGTTCGATGCC 2053	
REFERENCE		Hymenostomatida; Ophryogenina; Ichthyophthirius .		Qy 587 CTACTGGFACTGTACTGTGATGTTAGGGTGTGACACTTTTAATACATGCCACATTAT 646	
AUTHORS	Lin, Y., Lin, T.-L., Wang, C.-C., Wang, X., Stieger, K., Klopfleisch, R. and Clark, T.G.			Db 2054 CTGATGGTACTATAAGTCGTCGGAGT -- AAATATTGGTAGCACAAAACACTGAAT 2110	
1	(bases 1 to 3026)			Qy 647 GRTTAATGGCGACCTAACCTTTACTATAATGGTGTCCCTAAGTGAACCTCTG 706	
TITLE	Variation in primary sequence and tandem repeat copy number among 1-antigens of Ichthyophthirius multifiliis			Db 2111 GRACTAATTGGCTCTAACTTTTACAATAATAATGCTCTAATT----- 2155	
JOURNAL	Mol. Biochem. Parasitol. 120 (1), 93-106 (2002)			Qy 707 GCCTTAAAGTTGGCTGCTGGTGCCTGCGCTGCAAGTGTGGCTTCGGTTACTAGTTAAT 766	
MEDLINE	11839613			Db 2136 ----- JCAATCCAGTAAATGTCAT 2176	
PUBMED	11849709			Qy 767 GRTGCTCTTGCCAAATAAACAAAAAGGATCTCCCT--GCCACTGCGAGTGCCTAAGCTGA 823	
AUTHORS	Lin, Y., Lin, T.-L. and Clark, T.G.			Db 2177 GCCTACCTTGCCCAAGGAAATAAGATTATGTCGCTGAGGCAACTGCGCTTA 2236	
TITLE	Direct Submission			Qy 824 ATTAGGCACATAATGCGACTTAATGTCGCAACTGGCATTCAAGCGGATGGA 883	
JOURNAL	Submitted (27-Nov-2000) Microbiology and Immunology, NYSCMV Cornell University, Ithaca, NY 14853, USA			Db 2237 CTTAGCCAAATAATGTTAATTCGCTGCGCTGATGTCGAAATGCTCCCTGATG 2356	
FEATURES	Location/Qualifiers			Qy 884 CACTTGGTTTGTAGTAATTCATCCACATAATGTCGTTAATGCTGAACTTAATTCTTTTA 943	
SOURCE	1..3026			Db 2237 CTAATTTATGTTAAATATAACAGAAATGCTAAATTGTCGCTAACTTTTGTGATGCTGCTAATTTGATG 2356	
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	/macronuclear			Db 2337 GTAATAAATTCTAGGGAGGAGTACTAGTGTGCAAGATGTCGAAATAAAAGTTAAG 2416	
	/serotype= "D"			Qy 1001 CTCCACACATGCTCCAGTAATGCAACTTAATGTTGACCACTGTC 1060	
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	1285..1285			Db 2477 CTGCTGGTACTGTACTCACCGATGAAACAACTACATGTCGAAATAAAAGTTAAG 2536	
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Qy	718	TTGCTGGCTGGCTGGCTGGTGACTGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT	759
Db	49094	GGTGTGCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT	49053
RESULT	6		
LOCUS	AL365272	AL365272 Human DNA sequence from Clone RP11-328C17 on Chromosome 6, complete sequence.	
DEFINITION			
ACCESSION	AL365272.20	GR:11991402	
VERSION			
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. (bases 1 to 132449)	
REFERENCE	Heath, P.		
AUTHORS			
TITLE	Direct Submission		
JOURNAL	Submitted (23-DIC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail: enquiries@sanger.ac.uk		
COMMENT	requests: clonerequest@sanger.ac.uk		
	On Dec 24, 2000 this sequence version replaced g1:11875910.		
	During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.		
	This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the 'unsure' feature key, there is an annotation using the 'unsure' feature key.		
	The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:		
	Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WOMPEP; Information on the WOMPEP database can be found at		
	http://www.sanger.ac.uk/Projects/-ellegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at		
	http://www.sanger.ac.uk/HGP/Chr6 RP11-328C17 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see		
	http://chori.org/bacpac/home.htm		
VECTOR:	PBACE3.6		
IMPORTANT:	This sequence is not the entire insert of Clone RP11-328C17 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-328C17 is at 132449 in this sequence. The true left end of clone RP11-233k4 is at 64893 in this sequence. The true right end of clone RP3-416U7 is at 100 in this sequence. The true right end of clone RP1-125A24 is at 61243 in this sequence.		
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		23529..23642	/note="MLTIB repeat: matches 1. .12109 of consensus"
		23643..23756	/note="MLTIB repeat: matches 1. .12109 of consensus"
		23757..23870	/note="MLTIB repeat: matches 1. .12109 of consensus"
		23871..23984	/note="MLTIB repeat: matches 1. .12109 of consensus"
		23985..24108	/note="MLTIB repeat: matches 1. .12109 of consensus"
		24109..24222	/note="MLTIB repeat: matches 1. .12109 of consensus"
		24223..24336	/note="MLTIB repeat: matches 1. .12109 of consensus"
		24337..24450	/note="MLTIB repeat: matches 1. .12109 of consensus"
		24451..24564	/note="MLTIB repeat: matches 1. .12109 of consensus"
		24565..24678	/note="MLTIB repeat: matches 1. .12109 of consensus"
		24679..24792	/note="MLTIB repeat: matches 1. .12109 of consensus"

Db 102663 CTGCTACTCCCTGCCACAGCTACTGCAACTGCTGCTGCT 102640

RESULT	7	Center:	Baylor College of Medicine
LOCUS	AC099174/C	Center code:	BCM
DEFINITION	Rattus norvegicus clone CH230-9811, *** SEQUENCING IN PROGRESS ***,	Web site:	http://www.hgsc.bcm.edu/
ACCESSION	AC099174	Contact:	hgsc-help@bcm.tmc.edu
VERSION	HTG	-----	Project Information
KEYWORDS	Rattus norvegicus	Center project name:	GGZV
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Center clone name:	CH230-9811
ORGANISM	Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae;	-----	Summary Statistics
RATTUS	1 (bases 1 to 176822)	Sequencing vector:	Plasmid;
	Muzny, D.M., Adams, C.C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alstrooks, S.L., Amaralunghe, H.C., Are, J.R., Ayelle, M., Banks, T., Barbour, J., Benton, J., Bingham, K., Bonnici, D., Bouck, J., Bowie, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P., Buñay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Carrazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C., Cleaveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.-H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhaij, C., Escott, M., Fallis, T., Ferragut, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P.P., Hale, S., Harris, C., Harris, K., Hart, M., Havlik, P., Hawes, A., Hernandez, J., Hernandez, O., Hoagson, A., Hoque, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J.J., Hulyk, S., Hume, J.J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karatovic, J., Kelly, S., Khan, U., King, L., Korvaha, J., Kovar, C., Li, J., Li, Z., Lichchage, O., Lieu, C., Liu, J., Liu, W., Louissaged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, B., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, J., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Noser, M., Neal, D., Newtron, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokonkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I.I., Rolfe, M., Ruiz, S., Savy, G., Scherer, S., Scott, G., Shen, H., Shooshani, N., Siisson, I., Sodergren, E., Sonalkar, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatesk, A., Tabor, P., Tamerisa, A., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williamson, G., Williamson, J., Wu, Y., Wu, Y.-F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.	Chemistry:	Dye-Terminator Big Dye: 100% of reads
REFERENCE	1	Assembly program:	Phrap; version 0.190329
AUTHORS		Consensus quality:	115453 bases at least Q40
JOURNAL		Consensus quality:	125501 bases at least Q30
		Consensus quality:	133023 bases at least Q20
		-----	NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.edu/docs/Genbank_draft_data.html).
		NOTE:	This is a working draft sequence. It currently consists of 77 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
		1	1052: contig of 1052 bp in length
		*	1053: 1152: gap of unknown length
		*	1153: 2179: contig of 1027 bp in length
		*	2180: 2279: gap of unknown length
		*	2280: 3355: contig of 1076 bp in length
		*	3356: 3455: gap of unknown length
		*	3456: 4834: contig of 1379 bp in length
		*	4835: 4934: gap of unknown length
		*	4935: 6222: contig of 1288 bp in length
		*	6223: 6322: gap of unknown length
		*	6323: 7400: contig of 1078 bp in length
		*	7401: 7500: gap of unknown length
		*	7501: 8807: contig of 1307 bp in length
		*	8808: 8907: gap of unknown length
		*	8908: 10266: contig of 1359 bp in length
		*	10267: 10366: gap of unknown length
		*	10367: 11662: contig of 1296 bp in length
		*	11663: 11762: gap of unknown length
		*	11763: 12812: contig of 1050 bp in length
		*	12812: 12912: gap of unknown length
		*	12913: 14136: contig of 1224 bp in length
		*	14137: 14236: gap of unknown length
		*	14237: 15446: contig of 1210 bp in length
		*	15447: 15546: gap of unknown length
		*	15547: 16866: contig of 1320 bp in length
		*	16866: 16966: gap of unknown length
		*	16966: 18700: contig of 1734 bp in length
		*	18701: 18800: gap of unknown length
		*	18801: 20318: contig of 1558 bp in length
		*	20359: 20458: gap of unknown length
		*	20459: 22025: contig of 1567 bp in length
		*	22025: 22125: gap of unknown length
		*	22126: 24515: contig of 2390 bp in length
		*	24516: 24615: gap of unknown length
		*	24616: 25846: contig of 1231 bp in length
		*	25847: 25946: gap of unknown length
		*	25947: 27116: contig of 1230 bp in length
		*	27116: 27276: gap of unknown length
		*	27276: 28283: contig of 1007 bp in length
		*	28283: 28383: gap of unknown length
		*	28384: 29995: contig of 1612 bp in length
		*	29996: 30095: gap of unknown length
		*	30095: 31159: contig of 1364 bp in length
		*	31159: 31460: gap of unknown length
		*	31460: 32824: contig of 1365 bp in length
		*	32824: 33024: gap of unknown length
		*	33024: 33295: contig of 1049 bp in length
		*	33295: 34073: contig of 1049 bp in length
		*	34073: 34173: gap of unknown length

Chemistry: Dye-primer ET; 10% of reads
 Chemistry: Dye-terminator Big Dye; 0% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 17535 bases at least Q40
 Consensus quality: 17552 bases at least Q30
 Consensus quality: 17171 bases at least Q20
 Insert size: 198000; agarose-fp
 Insert size: 178453; sum-of-contigs
 Quality coverage: 4.48 in Q20 bases; agarose-fp
 Quality coverage: 4.99 in Q20 bases; sum-of-contigs
 NOTE: This is a 'working draft' sequence. It currently
 consists of 12 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

**	1	7554:	contig of 7554 bp in length
**	7555	7654:	gap of unknown length
**	7655	16350:	contig of 8695 bp in length
**	16350	16449:	gap of unknown length
**	16449	16450:	contig of 10026 bp in length
**	16450	26475:	gap of unknown length
**	26476	26575:	gap of 9305 bp in length
**	26575	35980:	contig of unknown length
**	35981	35980:	gap of unknown length
**	35980	62010:	contig of 26030 bp in length
**	62010	62110:	gap of unknown length
**	62110	90565:	contig of 28455 bp in length
**	90566	90665:	gap of unknown length
**	90666	117183:	contig of 26518 bp in length
**	117183	117283:	gap of unknown length
**	117283	163019:	contig of 45736 bp in length
**	163019	163119:	gap of unknown length
**	163119	166938:	contig of 3819 bp in length
**	166938	167039:	gap of unknown length
**	167039	169312:	contig of 2274 bp in length
**	169312	169412:	gap of unknown length
**	169412	171639:	contig of 2227 bp in length
**	171639	171739:	gap of unknown length
**	171739	179553:	contig of 7814 bp in length.

source

Db	175703	GGCTGCCTATTATGTTGCC	--TGCGTCTATTGCTGTGTTACGCTGTTATGTTGCTGT	175759
Qy	1050	GACCACATGCTGGTACAGTAGCTTGTGATGATGTCACAACTAATTTGCTGTTAC	TGCTGTTATGTTGCTGT	1109
Db	175760	TATGTTGGTATGCTGCTACTTAATGTTGCTGGCTATGTTGCTATGTTGCT	GTGCTATGTTGCTATGTTGCT	175819
Qy	1110	CGCAACTGAATGTTACTAAATGTTGCTGGCTATGTTGCTATGTTGCT	GTGCTATGTTGCTATGTTGCT	1169
Db	175820	TGCTGCTGCTACTGGTGTGCTGCTGCTACTGGTGTGCTGCTATGTTGCT	GTGCTATGTTGCTATGTTGCT	175879
Qy	1170	AGCGATGTTGATGATCAGTAACTGAAATGTTGCTGCTGCTATGTTGCT	GTGCTATGTTGCTATGTTGCT	1229
Db	175880	TGCGCTGCTGCTGCTGCTGCTGCTGCTGCTATGTTGCTATGTTGCT	GTGCTATGTTGCTATGTTGCT	175939
Qy	1230	AGTATATGCTGAAGCTACT	1248	
Db	175940	TGTTATTGCTGCGACTTGT	175958	
RESULT				
AC096032	AC096032	170985 bp DNA	linear	HTG 11-JUL-2002
LOCUS	Rattus norvegicus clone CH230-37D13, ***	SEQUENCING IN PROGRESS		
DEFINITION	76 unordered pieces.			
ACCESSION	AC096032			
VERSION	AC096032.4			
HTG,	HTGS, PHASEI.			
Norway rat.				
ORGANISM	Rattus norvegicus			
MATERIAL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
REFERENCE	1 (bases 1 to 170985)			
AUTHORS	Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaralungue, H.C., Are, J.J.R., Ayete, M., Banks, T., Barbara, J., Benton, J., Biimage, K., Blankenburg, K., Bonnici, D., Bouck, J., Bowies, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burkh, P., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carrion, T.F., Carter, M., Cavazos, S.R., Chacio, J., Chavez, D., Cheu, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyne, M.D., Dathorne, S.R., David, R., Dayila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.H., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, D., Edwards, C.C., Elhajj, C., Escott, M., Earthart, C., Edgar, D., Edwards, C.C., Elhajj, C., Jackson, L.E., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, C.A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunnaratre, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlik, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, K.J., Hulyk, S., Hume, C., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karrasik, E., Kelly, S., Khan, U., King, L., Korvai, C., Kovacs, C., Kratovics, J., Kureshi, A., Mandry, N., Leah, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichatoge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozada, R.J., Lu, X., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massy, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, J., Metzker, M., Miner, Z., Mitchell, T., Monhabot, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokonkwo, S., Oguh, M., Okwuonu, G., Orangune, N., Oviiedo, R., Pace, A., Payton, B., Perry, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.-L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rejubakan, I., Rolfe, M., Ruiz, S., Savery, G., Scheer, S., Scott, G., Shen, H., Shooshbati, N., Sisson, J., Sodergren, E., Sonalkar, T., Sparks, A., Stanley, H., Stone, H., Tang, H., Sutton, A., Svatek, A., Tabor, P., Tamlerisa, A., Tamlerisa, K., Tang, H., Tsuneyi, K., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, Y., Villafon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wickey, R., Woden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,			

TITLE Weinstock, G. and Gibbs, R.
 JOURNAL Direct Submission
 Unpublished
 2 (bases 1 to 170985)
 REFERENCE Worley, K.C.
 AUTHORS Direct Submission
 Submitted (17-SEP-2001) H
 of Molecular and Human Ge
 Baylor Plaza, Houston, TX
 3 (bases 1 to 170985)
 REFERENCE Worley, K.C.
 AUTHORS Direct Submission
 Submitted (11-JUL-2002) H
 of Molecular and Human Ge
 Baylor Plaza, Houston, TX
 On Jul 10, 2002 this sequ
 Center: Baylor College
 Center code: BCM
 Web site: <http://www.hgsc>
 Contact: hgsc-help@hgsc
 Project: Human Genome Project
 Center project name:
 Center clone name: cH
 Sequencing vector: pCR2.1-TOPO
 Chemistry: dye-terminator
 Assembly program: Phred
 Consensus quality: 11
 Consensus quality: 11
 Consensus quality: 11
 Consensus quality: 11
 * NOTE: Estimated insert
 * (see <http://www.hgsc>)
 * NOTE: This is a 'workin
 * consists of 76 contigs
 * is not known and their
 * arbitrary. Gaps between
 * runs of N, but the exacta
 * This record will be upda
 * as soon as it is availab
 * be preserved.
 * 1416: con
 * 1417 1516: gap
 * 1517 2771: con
 * 2772 2871: gap
 * 2872 4128: con
 * 4129 4428: gap
 * 4430 5433: con
 * 5434 5533: gap
 * 5534 6884: con
 * 6885 6984: gap
 * 6985 8084: con
 * 8085 8184: gap
 * 8185 9251: con
 * 9254 9333: gap
 * 9354 10956: con
 * 10957 11056: gap
 * 11057 12330: con
 * 12321 12440: gap
 * 12421 13487: con
 * 13488 13587: gap
 * 13588 14607: con
 * 14608 14707: gap
 * 14708 15871: con
 * 15872 15971: gap
 * 15972 17730: con
 * 17751 17850: gap
 * 17851 19143: con
 * 19150 19249: gap
 * 19250 21237: con
 * 21337: 969
 * 21338 22459: con
 * 21339 22459: con

REFERENCE 2 (bases 1 to 186935)

AUTHORS Waterston, R.H.

TITLE Direct Submission

JOURNAL Submitted (30-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT On Mar 24, 2000 this sequence version replaced gi:7109575.

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site:<http://genome.wustl.edu/gsc/index.shtml>

Project Information -----

Center project name: H_NH0317M22

Summary Statistics -----

Sequencing vector: M13; 100%

Sequencing vector: plasmid; 0%

Chemistry: dye-primer ET; 100% of reads

Chemistry: Dye-terminator Big Dye; 0% of reads

Assembly program: Phrap; version 0.99019

Consensus quality: 181940 bases at least Q40

Consensus quality: 183253 bases at least Q30

Consensus quality: 183774 bases at least Q20

Insert size: 186000; agarose-fp

Insert size: 185435; sum-of-contigs

Quality coverage: 6.94 in Q20 bases; agarose-fp

Quality coverage: 7.00 in Q20 bases; sum-of-contigs

* NOTE: This is a "working draft" sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 1363: contig of 1363 bp in length

* 1464 1463: gap of unknown length

* 3253: contig of 1790 bp in length

* 3254 3353: gap of unknown length

* 3354 4598: contig of 1245 bp in length

* 4599 4698: gap of unknown length

* 4699 5833: contig of 1135 bp in length

* 5834 5933: gap of unknown length

* 5934 8646: contig of 2713 bp in length

* 8647 8746: gap of unknown length

* 8747 11792: contig of 3046 bp in length

* 11793 11892: gap of unknown length

* 14813: contig of 2921 bp in length

* 14914 14913: gap of unknown length

* 14914 19837: contig of 4924 bp in length

* 19938 19938: gap of unknown length

* 24772: contig of 4835 bp in length

* 24873: gap of unknown length

* 30965: contig of 6093 bp in length

* 31066: gap of unknown length

* 31066 40842: contig of 9776 bp in length

* 40842 52859: gap of unknown length

* 52870 52899: gap of unknown length

* 63636 63735: contig of 10666 bp in length

* 63736 63736: gap of unknown length

* 90222 90323: contig of 11928 bp in length

* 90323 135922: gap of unknown length

* 135922 136021: contig of 45599 bp in length

* 136022 186935: contig of 50914 bp in length.

Location/Qualifiers 1. 186935

FEATURES source

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="6"

/clone="RP11-317M22"

*	101409	101508:	gap of unknown length	
*	101509	104411:	contig of 2903 bp in length	
Query Match	6.78%	Score 88.4 -	DB 2;	Length 191841;
Best Local Similarity	45.3%	Pred. No. 2, 2e-07;		
Matches 320;	Conservative 0;	Mismatches 386;	Indels 0;	Gaps 0;
Db 141576	AAGAGTTTGCATGTCCTGATGGTACTCTAGACTCAAGCTGGATTGACTGATGTAGTGTC	113		
Qy 54	AGAGCTGTCCATGTCCTGATGGTACTCTAGACTCAAGCTGGATTGACTGATGTAGTGTC	113		
Db 141636	TGCTGATCTGGTACTGTGTTAATTCGAGCTTAATTTACTATAATGGTGTGCTGTC	173		
Qy 114	TGCTGATCTGGTACTGTGTTAATTCGAGCTTAATTTACTATAATGGTGTGCTGTC	173		
Db 141636	TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	141695		
Qy 174	TAAAGGAGAGCTTAATGCTTAACCTTTCGCGCAAATAAATGGCTAGAGGTATATG	233		
Db 141696	TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	141755		
Qy 234	TGTACCATGCCAATAAACAGAGTAGGCTCTGTTACCAATGGAGGTGACTTAGCTACTTT	293		
Db 141756	TATGTGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	141815		
Qy 294	AGCCACATATGCGAGTACTTAATGCTCCTACTGGCACTGGCACTTGATGGTACAGA	353		
Db 141816	TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	141875		
Qy 354	TGTTTTGATAGATCAGCGCCATAATGTTAATGCAAACCTTAACCTTACTATAATGG	413		
Db 141876	TGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	141935		
Qy 414	TGGTTCTCTTAACTGTGAGCTCTGGCCTTAAGTTTGCTGCTGCTGCTGCTGCTG	473		
Db 141936	TGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	141995		
Qy 474	AGGCTACTGGTGGCCGTTACTAGTTAATGCTACCTTGCAACTAAACAAACATTCTC	533		
Db 141996	TGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	142055		
Qy 534	TGCCACTGGAGGTGCTTAAGCTTAATTAGCCACATAATGCAATTAAATGTCCTACTG	593		
Db 142056	TGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	142115		
Qy 594	CACGTACTGTGATGTTGAGTGTGACTGTTTAATAGATCACGCCAAATTGCTGTT	653		
Db 142116	TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	142175		
Qy 654	ATGAGACACTTAACCTTTACTATAATGGTGTCTCTTAAAGCTGAAGCTCTGGCTT	713		
Db 142176	TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	142235		
Qy 714	AGTTTTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGTACT	759		
Db 142236	TGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	142281		
RESULT 1.3				
AC110817	AC110817	204259 bp	DNA linear	HTG 29-JUL-2002
LOCUS	Mus musculus chromosome UNK clone RP23-155B20,			WORKING DRAFT
DEFINITION	SEQUENCE, 16 unordered pieces.			
ACCESSION	AC110817			
VERSION	AC110817.3	GI:21105087		
KEYWORDS	HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia: Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 20459)			
AUTHORS	McPherson, J.D. and Waterston, R.H.			
TITLE	The sequence of <i>Mus musculus</i> clone			
JOURNAL	Unpublished			
REMARKS	2 (bases 1 to 20459)			

AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 3 (bases 1 to 20459)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT On May 23, 2002 this sequence version replaced gi:18874253.

Center : Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site:<http://genome.wustl.edu/gsc/index.shtml>
 Contact: submissions@wustl.edu

Project : Project Information
 Center project name: M_BA0155B20

Summary Statistics

Sequencing vector: M13, 08
 Sequencing vector: plasmid; 100%
 Chemistry: Dye-primer ET; 0% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 198852 bases at least Q40
 Consensus quality: 200032 bases at least Q30
 Consensus quality: 201011 bases at least Q20
 Insert size: 211000; agarose-fp
 Insert size: 203242; sum-of-contigs
 Quality coverage: 8.38 in 200 bases; agarose-fp
 Quality coverage: 8.78 in 020 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1226: contig of 1226 bp in length
 * 1227 1326: gap of unknown length
 * 1327 2375: contig of 1049 bp in length
 * 2376 2475: gap of unknown length
 * 2476 3800: contig of 1325 bp in length
 * 3801 3900: gap of unknown length
 * 3901 5876: contig of 1976 bp in length
 * 5877 5976: gap of unknown length
 * 5977 7869: contig of 1893 bp in length
 * 7870 7969: gap of unknown length
 * 7970 9641: contig of 1672 bp in length
 * 9642 9741: gap of unknown length
 * 9742 14703: contig of 4962 bp in length
 * 14704 14803: gap of unknown length
 * 14804 20620: contig of 5817 bp in length
 * 20621 20720: gap of unknown length
 * 20721 30399: contig of 9669 bp in length
 * 30390 30489: gap of unknown length
 * 30490 38838: contig of 8349 bp in length
 * 38839 38938: gap of unknown length
 * 38939 51519: contig of 12581 bp in length
 * 51520 51619: gap of unknown length
 * 51620 70098: contig of 18479 bp in length
 * 70099 70198: gap of unknown length
 * 30499 100939: contig of 30741 bp in length
 * 100940 101039: gap of unknown length
 * 101040 131732: contig of 30693 bp in length
 * 131733 131832: gap of unknown length
 * 131833 163281: contig of 32049 bp in length
 * 163282 163981: gap of unknown length
 * 163982 204259: contig of 40278 bp in length
 * Location/Qualifiers

Search completed: February 16, 2003, 20:52:51
Job time : 4000.67 secs